

1 ATGAAGTTGCCCTGTTAGGCTGTTGGTGCTCTGTTCTGGATTCCCTGTTCCGGAGGT 60

 1 TACTTCAACGGACAATCCGACAACCACGAAGACAACAAGACCTAAGGACAAAGGCCTCCA
 [M K L P V R L L V L L L F W I P V S G G]
 signal Peptide

61 GATGTTGTGGTGAUTCAAACCTCCACTCTCCCTGCCTGTCAGCTTGGAGATCAAGTTCT 120

 61 CTACAACACCACGTGAGTTGAGGTGAGAGGGACGGACAGTCGAAACCTCTAGTTCAAAGA
 [D V V V T Q T P L S L P V S F G D Q V S]
 Framework 1

121 ATCTCTTGCAGGTCTAGTCAGAGTCTTCAAAGAGTTATGGGAACACCTATTGTCTTGG 180

 121 TAGAGAACGTCCAGATCAGTCTCAGAACGTTCTCAATACCCCTGTTGATAAACAGAAC
 [I S C][R S S Q S L A K S Y G N T Y L S][W]
 CDR 1

181 TACCTGCACAAGCCTGGCCAGTCTCCACAGCTCCTCATCTATGGGATTCCAACAGATT 240

 181 ATGGACGTGTTGGACCGGTCAAGGTGTCGAGGAGTAGATACCCCTAAAGGTGTCTAAA
 [Y L H K P G Q S P Q L L I Y][G I S N R F]
 Framework 2 CDR 2

241 TCTGGGTGCCAGACAGGTTCACTGGCAGTGGTTCAAGGGACAGATTCACACTCAAGATC 300

 241 AGACCCCCACGGTCTGTCAGTCACCGTCACCAAGTCCCTGTCATAAGGTGTGAGTTCTAG
 [S][G V P D R F S G S G S G T D F T L K I]
 Framework 3

301 AGCACACAATAAGCCTGAGGACTTGGGAATGTATTACTGCTTACAAGGTACACATCAGCCG 360

 301 TCGTGTATTTCGGACTCCTGAACCCCTACATAATGACGAATGTTCCATGTGTAGTCGGC
 [S T I K P E D L G M Y Y C][L Q G T H Q P]
 CDR 3

361 TACACGTTGGAGGGGGACCAAGCTGGAAATAAAA

 361 ATGTGCAAGCCTCCCCCCTGGTCGACCTTTATT
 [Y T][F G G G T K L E I K]
 Framework 4

ATGGGATGGAGCTGTATCATCCTCTTGGTATCAACAGCTACAAGTGTCCACTCCCAG 60
1 -----
TACCCCTACCTCGACATAGTAGGAGAAGAACCATAGTTGTCGATGTTCACAGGTGAGGGTC
M G W S C I I L F L V S T A T S V H S][Q

Signal Peptide

GTCCAAC TGCAG CAG C CTGGGCTGAG CTTGTGAAGCCTGGGACTTCAGTGAAGCTGTCC 120
61 -----
CAGGTTGACGTCGTCGGACCCCGACTCGAACACTTCGGACCCTGAAGTCAC TCGACAGG
V Q L Q Q P G A E L V K P G T S V K L S

Framework 1

TGCAAGGGTTATGGCTACACCTTACCCAGCTACTGGATGCACTGGGTGAAGCAGAGGCCT 180
121 -----
ACGTTCCCAATACCGATGTGGAAAGTGGTCGATGACCTACGTGACCCACTCGTCTCCGGA
C K G Y G Y T F T][S Y W M H][W V K Q R P

CDR 1

GGACAAGGCCTTGAGTGGATCGGAGAGATTGATCCTTCTGAGAGTAATACTAACTACAAT 240
181 -----
CCTGTTCCGGAAC T CACCTAGCCTCTCTAACTAGGAAGACTCTCATTATGATTGATGTTA
G Q G L E W I G][E I D P S E S N T N Y N

Framework 2 CDR 2

CAAAATTCAAGGGCAAGGCCACATTGACTGTAGACATTCCCTCCAGCACAGCCTACATG 300
241 -----
GTTTTTAAGTCCCGTTCCGGTGTAACTGACATCTGTAAAGGAGGTGCTGTCGGATGTAC
Q K F K G][K A T L T V D I S S S T A Y M

Framework 3

CAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTACTATTGTCAAGAGGGGGTTAC 360
301 -----
GTCGAGTCGTCGGACTGTAGACTCCTGAGACGCCAGATGATAACACGTTCTCCCCCAATG
Q L S S L T S E D S A V Y Y C A R][G G Y

GACGGATGGGACTATGCTATTGACTACTGGGGTCAAGGCACCTCAGTCACCGTCTCCTCA 420
361 -----
CTGCCTACCCCTGATACTGACATGACCCAGTTCCGTGGAGTCAGTGGCAGAGGAGT
D G W D Y A I D Y][W G Q G T S V T V S S]

CDR 3 Framework 4

10 20 30 40

* * * *

ATG AAA TGC ACC TGG GTC ATT CTC TTC TTG GTA TCA ACA GCT ACA AGT

M K C T W V I L F L V S T A T S>

signal peptide cleavage site

50 60 70 80 90

* * *| Spe I* * * *

GTC CAC TCC CAG GTC CAA CTA GTG CAG TCT GGG GCT GAG GTT AAG AAG

V H S Q V Q| L V Q S G A E V K K

100 110 120 130 140

* * * * *

CCT GGG GCT TCA GTG AAG GTG TCC TGC AAG GGT TCT GGC TAC ACC TTC

P G A S V K V S C K G S G Y T F>

Xba I

150 160 170 180 190

* * * * *

ACC AGC TAC TGG ATG CAT TGG GTG AGG CAG GCG CCT GGC CAA CGT CTA

T S Y W M H W V R Q A P G Q R| L>

200 210 220 230 240

* * * * *

GAG TGG ATC GGA GAG ATT GAT CCT TCT GAG AGT AAT ACT AAC TAC AAT

E W I G E I D P S E S N T N Y N>

250 260 270 280 Nhe I

* * * * *

CAA AAA TTC AAG GGA CGC GTC ACA TTG ACT GTA GAC ATT TCC| GCT AGC

Q K F K G R V T L T V D I S| A S>

290 300 310 320 330

* * * * *

ACA GCC TAC ATG GAG CTC AGC AGC CTG AGA TCT GAG GAC ACT GCG GTC

T A Y M E L S S L R S E D T A V>

340 350 360 370 380

* * * * *

TAC TAT TGT GCA AGA GGG GGT TAC GAC GGA TGG GAC TAT GCT ATT GAC

Y Y C A R G G Y D G W D Y A I D>

390 400 410 420 Constant 430

* * * * *region*

TAC TGG GGT CAA GGC ACC CTG GTC ACC| GTC TCC TCA| GCC TCC ACC AAG

Y W G Q G T L| V T| V S S A S T K>

440 450 460 470 480

* * * * *

GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG

G P S V F P L A P S S K S T S G>

490 500 510 520

* * * * *

GGC ACA GCG GCC CTG GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG

G T A A L G C L V K D Y F P E| P>

530 540

*| *| *

GTG ACG GTG TCG| V| T V S>

	10	20	30	40												
*	*	*	*	*	*											
ATG	AAG	TTG	CCT	GTT	AGG	CTG	TTG	GTG	CTT	CTG	TTG	TTC	TGG	ATT	CCT	
M	K	L	P	V	R	L	L	V	L	L	L	F	W	I	P>	
Signal peptide cleavage site																
50	<u>BspE I</u>	60		70		80		90								
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
GTT	TCC	GGA	GGT	GAT	GTT	GTG	ATG	ACT	CAA	AGT	CCA	CTC	TCC	CTG	CCT	
V	<u>S</u>	<u>G</u>	G	D	V	V	M	T	Q	S	P	L	S	L	P>	
	100	110	120	130	140											
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
GTC	ACC	CCT	GGA	GAA	CCA	GCT	TCT	ATC	TCT	TGC	AGG	TCT	AGT	CAG	AGT	
V	T	P	G	E	P	A	S	I	S	C	R	S	S	Q	S>	
	150	160	170	180	Asp 718	190										
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
CTT	GCA	AAG	AGT	TAT	GGG	AAC	ACC	TAT	TTG	TCT	TGG	TAC	CTG	CAG	AAG	
L	A	K	S	Y	G	N	T	Y	L	S	<u>W</u>	<u>Y</u>	L	Q	K>	
	200	210	220	230	240											
*	<u>Msc I</u>	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
CCT	GGC	CAG	TCT	CCA	CAG	CTC	CTC	ATC	TAT	GGG	ATT	TCC	AAC	AGA	TTT	
P	G	Q	S	P	Q	L	L	I	Y	G	I	S	N	R	F>	
	250	260	270	280												
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
TCT	GGG	GTG	CCA	GAC	AGG	TTC	AGT	GGC	AGT	GGT	TCA	GGG	ACA	GAT	TTC	
S	G	V	P	D	R	F	S	G	S	G	S	G	T	D	F>	
	290	300 NruI	310	320	330											
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
ACA	CTC	AAG	ATC	<u>TCG</u>	<u>CGA</u>	GTA	GAG	GCT	GAG	GAC	GTG	GGA	GTG	TAT	TAC	
T	L	K	I	<u>S</u>	<u>R</u>	V	E	A	E	D	V	G	V	Y	Y>	
	340	350	360	370	380											
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
TGC	TTA	CAA	GGT	ACA	CAT	CAG	CCG	TAC	ACG	TTC	GGA	CAG	GGG	ACC	AAG	
C	L	Q	G	T	H	Q	P	Y	T	F	G	Q	G	T	K>	
	390	400	410 Kas I													
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	
GTG	GAA	ATA	AAA	CGG	GCT	GAT	GCG	GCG	CC							
V	E	I	K	R	A	D	A	<u>A</u>	<u>P></u>							

FIG. 4

Light Chain

CDR1 R S S Q S L A K S Y G N T Y L S
CDR2 G I S N R F S
CDR3 L Q G T H Q P Y T

Heavy Chain

CDR1 S Y W M H
CDR2 E I D P S E S N T N Y N Q K F K G
CDR3 G G Y D G W D Y A I D Y

FIG. 5

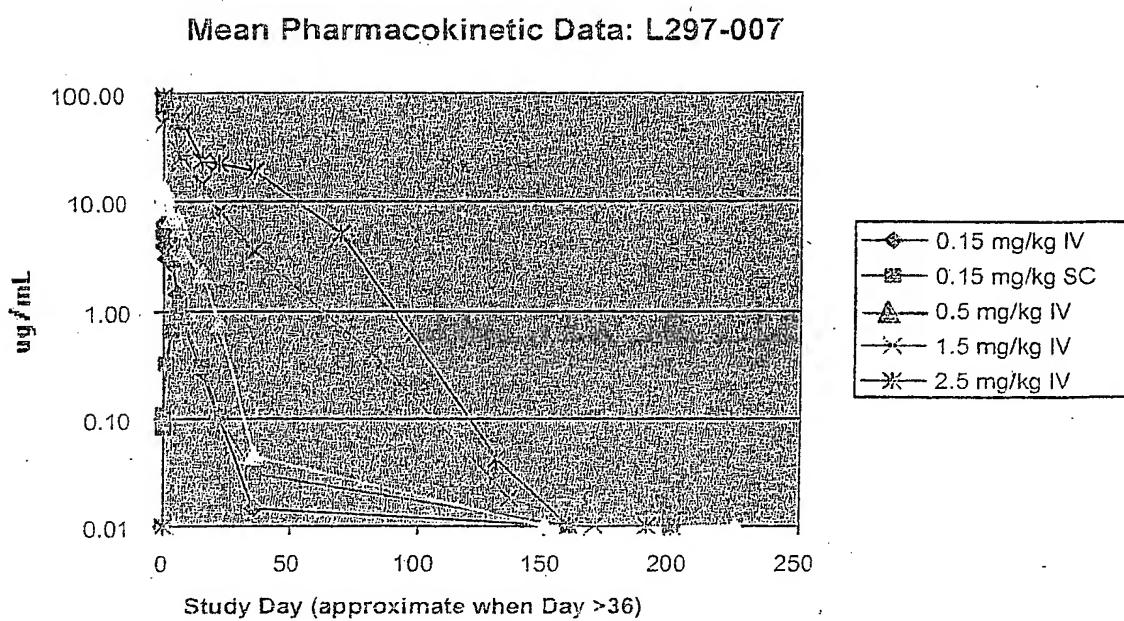


FIG. 6

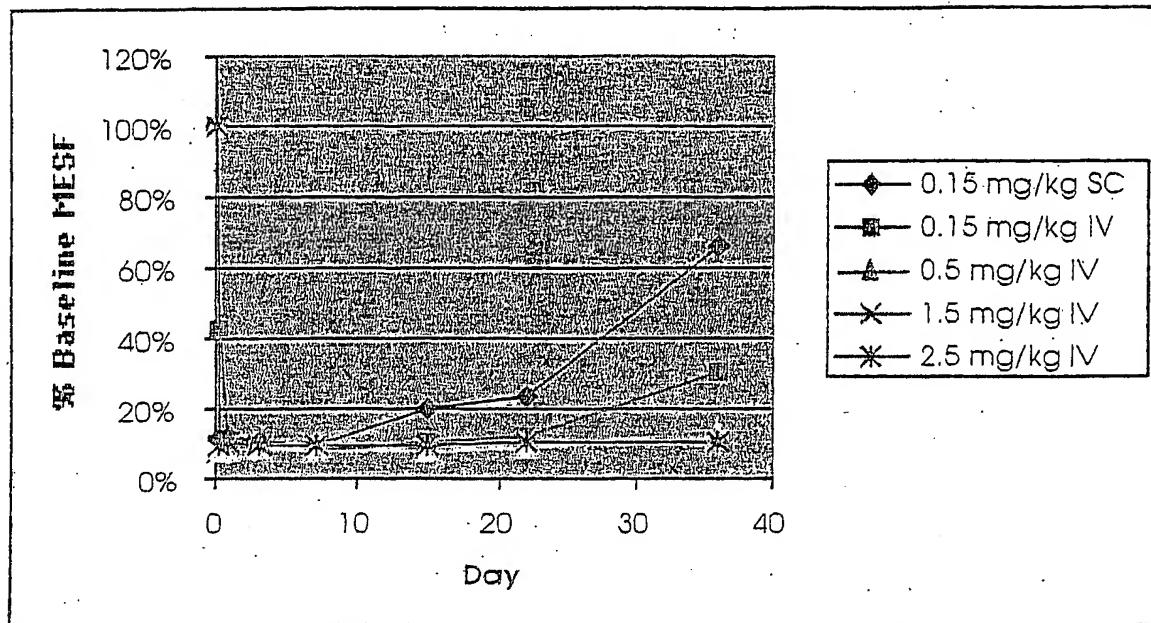


FIG. 7

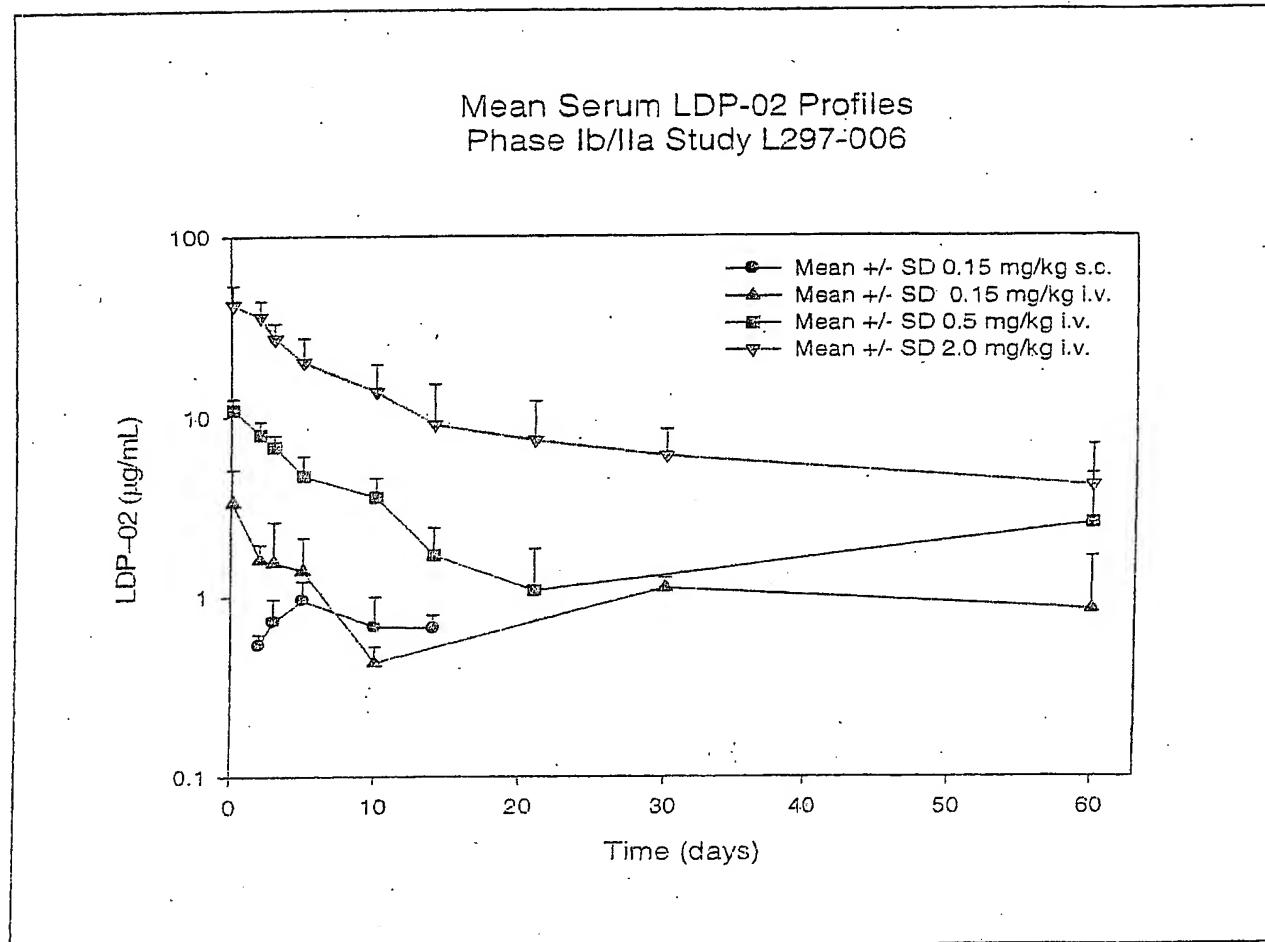


FIG. 8

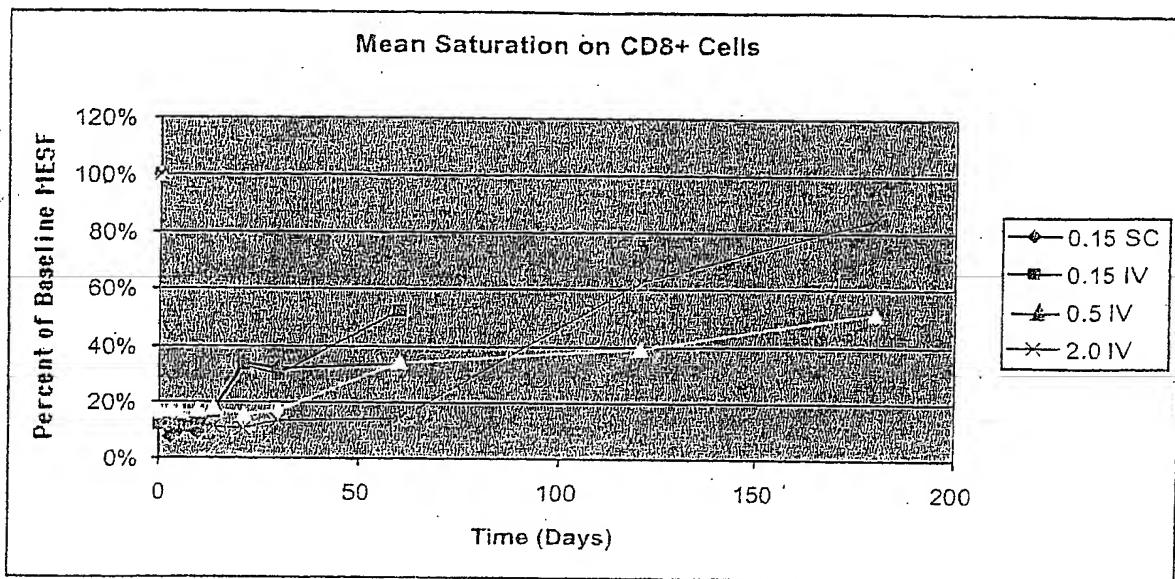


FIG. 9